



SEQUENCE LISTING

#4  
RECEIVED  
OCT 09 2001  
TECH CENTER 1600/2900

Wands, Jack R.  
de la Monte, Suzanne M.  
Ince, Nedim  
Carlson, Rolf I.

<120> DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

<130> 21486-032 DIV4

<140> 09/903,199

<141> 2001-07-11

<150> 09/436,184

<151> 1999-11-08

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
EGF-like domain

<220>

<221> VARIANT

<222> (2)..(8)

<223> Wherein Xaa is any amino acid

<220>

<221> VARIANT

<222> (10)..(13)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (15)..(24)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (26)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (28)..(35)

<223> Wherein Xaa is any amino acid.

<400> 1

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa  
20 25 30

Xaa Xaa Xaa Cys  
35

<210> 2

<211> 758

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Gln Arg Lys Asn Ala Lys Ser Ser Gly Asn Ser Ser Ser Ser  
1 5 10 15

Gly Ser Gly Ser Gly Ser Thr Ser Ala Gly Ser Ser Ser Pro Gly Ala  
20 25 30

Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly  
35 40 45

Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu  
50 55 60

Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr  
65 70 75 80

Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly  
85 90 95

Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg  
100 105 110

Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr  
115 120 125

Glu	Pro	Glu	Glu	Gln	Val	Pro	Val	Glu	Ala	Glu	Pro	Gln	Asn	Ile	Glu	130	135	140	
Asp	Glu	Ala	Lys	Glu	Gln	Ile	Gln	Ser	Leu	Leu	His	Glu	Met	Val	His	145	150	155	160
Ala	Glu	His	Val	Glu	Gly	Glu	Asp	Leu	Gln	Gln	Glu	Asp	Gly	Pro	Thr	165	170	175	
Gly	Glu	Pro	Gln	Gln	Glu	Asp	Asp	Glu	Phe	Leu	Met	Ala	Thr	Asp	Val	180	185	190	
Asp	Asp	Arg	Phe	Glu	Thr	Leu	Glu	Pro	Glu	Val	Ser	His	Glu	Glu	Thr	195	200	205	
Glu	His	Ser	Tyr	His	Val	Glu	Glu	Thr	Val	Ser	Gln	Asp	Cys	Asn	Gln	210	215	220	
Asp	Met	Glu	Glu	Met	Met	Ser	Glu	Gln	Glu	Asn	Pro	Asp	Ser	Ser	Glu	225	230	235	240
Pro	Val	Val	Glu	Asp	Glu	Arg	Leu	His	His	Asp	Thr	Asp	Asp	Val	Thr	245	250	255	
Tyr	Gln	Val	Tyr	Glu	Glu	Gln	Ala	Val	Tyr	Glu	Pro	Leu	Glu	Asn	Glu	260	265	270	
Gly	Ile	Glu	Ile	Thr	Glu	Val	Thr	Ala	Pro	Pro	Glu	Asp	Asn	Pro	Val	275	280	285	
Glu	Asp	Ser	Gln	Val	Ile	Val	Glu	Glu	Val	Ser	Ile	Phe	Pro	Val	Glu	290	295	300	
Glu	Gln	Gln	Glu	Val	Pro	Pro	Glu	Thr	Asn	Arg	Lys	Thr	Asp	Asp	Pro	305	310	315	320
Glu	Gln	Lys	Ala	Lys	Val	Lys	Lys	Lys	Lys	Pro	Lys	Leu	Leu	Asn	Lys	325	330	335	
Phe	Asp	Lys	Thr	Ile	Lys	Ala	Glu	Leu	Asp	Ala	Ala	Glu	Lys	Leu	Arg	340	345	350	
Lys	Arg	Gly	Lys	Ile	Glu	Glu	Ala	Val	Asn	Ala	Phe	Lys	Glu	Leu	Val	355	360	365	
Arg	Lys	Tyr	Pro	Gln	Ser	Pro	Arg	Ala	Arg	Tyr	Gly	Lys	Ala	Gln	Cys	370	375	380	

Glu Asp Asp Leu Ala Glu Lys Arg Arg Ser Asn Glu Val Leu Arg Gly  
 385 390 395 400  
 Ala Ile Glu Thr Tyr Gln Glu Val Ala Ser Leu Pro Asp Val Pro Ala  
 405 410 415  
 Asp Leu Leu Lys Leu Ser Leu Lys Arg Arg Ser Asp Arg Gln Gln Phe  
 420 425 430  
 Leu Gly His Met Arg Gly Ser Leu Leu Thr Leu Gln Arg Leu Val Gln  
 435 440 445  
 Leu Phe Pro Asn Asp Thr Ser Leu Lys Asn Asp Leu Gly Val Gly Tyr  
 450 455 460  
 Leu Leu Ile Gly Asp Asn Asp Asn Ala Lys Lys Val Tyr Glu Glu Val  
 465 470 475 480  
 Leu Ser Val Thr Pro Asn Asp Gly Phe Ala Lys Val His Tyr Gly Phe  
 485 490 495  
 Ile Leu Lys Ala Gln Asn Lys Ile Ala Glu Ser Ile Pro Tyr Leu Lys  
 500 505 510  
 Glu Gly Ile Glu Ser Gly Asp Pro Gly Thr Asp Asp Gly Arg Phe Tyr  
 515 520 525  
 Phe His Leu Gly Asp Ala Met Gln Arg Val Gly Asn Lys Glu Ala Tyr  
 530 535 540  
 Lys Trp Tyr Glu Leu Gly His Lys Arg Gly His Phe Ala Ser Val Trp  
 545 550 555 560  
 Gln Arg Ser Leu Tyr Asn Val Asn Gly Leu Lys Ala Gln Pro Trp Trp  
 565 570 575  
 Thr Pro Lys Glu Thr Gly Tyr Thr Glu Leu Val Lys Ser Leu Glu Arg  
 580 585 590  
 Asn Trp Lys Leu Ile Arg Asp Glu Gly Leu Ala Val Met Asp Lys Ala  
 595 600 605  
 Lys Gly Leu Phe Leu Pro Glu Asp Glu Asn Leu Arg Glu Lys Gly Asp  
 610 615 620  
 Trp Ser Gln Phe Thr Leu Trp Gln Gln Gly Arg Arg Asn Glu Asn Ala  
 625 630 635 640

Cys Lys Gly Ala Pro Lys Thr Cys Thr Leu Leu Glu Lys Phe Pro Glu  
645 650 655

Thr Thr Gly Cys Arg Arg Gly Gln Ile Lys Tyr Ser Ile Met His Pro  
660 665 670

Gly Thr His Val Trp Pro His Thr Gly Pro Thr Asn Cys Arg Leu Arg  
675 680 685

Met His Leu Gly Leu Val Ile Pro Lys Glu Gly Cys Lys Ile Arg Cys  
690 695 700

Ala Asn Glu Thr Arg Thr Trp Glu Glu Gly Lys Val Leu Ile Phe Asp  
705 710 715 720

Asp Ser Phe Glu His Glu Val Trp Gln Asp Ala Ser Ser Phe Arg Leu  
725 730 735

Ile Phe Ile Val Asp Val Trp His Pro Glu Leu Thr Pro Gln Gln Arg  
740 745 750

Arg Ser Leu Pro Ala Ile  
755

<210> 3

<211> 2324

<212> DNA

<213> Homo sapiens

<400> 3

cggaccgtgc aatggcccag cgtaagaatg ccaagagcag cggcaacagc agcagcagcg 60  
gctccggcag cggtagcacg agtgcgggca gcagcagccc cggggcccg agagagacaa 120  
agcatggagg acacaagaat gggaggaaaag gcggactctc gggaacttca ttcttcacgt 180  
ggtttatggt gattgcattg ctgggcgtct ggacatctgt agctgtcgtt tggtttgatc 240  
ttgttgacta tgaggaagtt ctaggaaaac taggaatcta tgatgctgat ggtgatggag 300  
atattgatgt ggatgatgcc aaagttttat taggacttaa agagagatct acttcagagc 360  
cagcagtcgc gccagaagag gctgagccac aactgagcc cgaggagcag gttcctgtgg 420  
aggcagaacc ccagaatatc gaagatgaag caaaagaaca aattcagtc cttctccatg 480  
aatggtaca cgcagaacat gttgaggag aagacttgca acaagaagat ggaccacag 540  
gagaaccaca acaagaggat gatgagtttc ttatggcgac tgatgtagat gatagatttg 600  
agaccctgga acctgaagta tctcatgaag aaaccgagca tagttaccac gtggaagaga 660  
cagtttcaca agactgtaat caggatatgg aagagatgat gtctgagcag gaaaatccag 720  
attccagtga accagtagta gaagatgaaa gattgcacca tgatacagat gatgtaacat 780  
accaagtcta tgaggaacaa gcagtatatg aacctctaga aaatgaaggg atagaaatca 840  
cagaagtaac tgctccccct gaggataatc ctgtagaaga ttcacaggta attgtagaag 900  
aagtaagcat ttttcctgtg gaagaacagc aggaagtacc accagaaaca aatagaaaaa 960  
cagatgatcc agaacaaaaa gcaaaagtta agaaaaagaa gcctaaactt ttaaataaat 1020

```

ttgataagac tattaaagct gaacttgatg ctgcagaaaa actccgtaaa aggggaaaaa 1080
ttgaggaagc agtgaatgca tttaaagaac tagtacgcaa ataccctcag agtccacgag 1140
caagatatgg gaaggcgagc tgtgaggatg atttggctga gaagaggaga agtaatgagg 1200
tgctacgtgg agccatcgag acctaccaag aggtggccag cctacctgat gtccctgcag 1260
acctgctgaa gctgagtttg aagcgctcgt cagacaggca acaatttcta ggtcatatga 1320
gaggttccct gcttaccctg cagagattag ttcaactatt tcccaatgat acttccttaa 1380
aaaatgacct tggcgtggga tacctcttga taggagataa tgacaatgca aagaaagttt 1440
atgaagaggt gctgagtgtg acacctaata atggctttgc taaagtccat tatggcttca 1500
tcctgaaggc acagaacaaa attgctgaga gcatcccata tttaaaggaa ggaatagaat 1560
ccggagatcc tggcactgat gatgggagat tttatttcca cctgggggat gccatgcaga 1620
gggttgggaa caaagaggca tataagtggg atgagcttgg gcacaagaga ggacactttg 1680
catctgtctg gcaacgctca ctctacaatg tgaatggact gaaagcacag ccttgggtgga 1740
cccaaaaaga aacgggctac acagagttag taaagtctt agaaagaaac tggaaagttaa 1800
tccgagatga aggccttgca gtgatggata aagccaaagg tctcttcctg cctgaggatg 1860
aaaacctgag ggaaaaaggg gactggagcc agttcacgct gtggcagcaa ggaagaagaa 1920
atgaaaatgc ctgcaaagga gctcctaaaa cctgtacctt actagaaaag ttccccgaga 1980
caacaggatg cagaagagga cagatcaaat attccatcat gcaccccggg actcacgtgt 2040
ggccgcacac agggcccaca aactgcaggc tccgaatgca cctgggcttg gtgattccca 2100
aggaaggctg caagattcga tgtgccaacg agaccaggac ctgggaggaa ggcaaggtgc 2160
tcacttttga tgactccttt gagcacgagg tatggcagga tgcctcatct ttccggctga 2220
tattcatcgt ggatgtgtgg catccggaac tgacaccaca gcagagacgc agccttccag 2280
caatttagca tgaattcatg caagcttggg aaactctgga gaga 2324

```

<210> 4

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: EGF-like  
cysteine-rich repeat

<220>

<221> VARIANT

<222> (3)..(5)

<223> Wherein any Xaa may be any amino acid

<220>

<221> VARIANT

<222> (6)..(7)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (10)

<223> Wherein Xaa is any amino acid.

<220>  
 <221> VARIANT  
 <222> (14)  
 <223> Wherein Xaa is any amino acid.

<220>  
 <221> VARIANT  
 <222> (17)..(18)

<220>  
 <221> VARIANT  
 <222> (25)..(26)  
 <223> Wherein Xaa is any amino acid.

<220>  
 <221> VARIANT  
 <222> (29)  
 <223> Wherein Xaa is any amino acid.

<400> 4  
 Cys Asp Xaa Xaa Xaa Cys Xaa Xaa Lys Xaa Gly Asn Gly Xaa Cys Asp  
 1 5 10 15  
 Xaa Xaa Cys Asn Asn Ala Ala Cys Xaa Xaa Asp Gly Xaa Asp Cys  
 20 25 30

<210> 5  
 <211> 1242  
 <212> PRT  
 <213> Homo sapiens

<400> 5  
 Met Ala Ser Pro Pro Glu Ser Asp Gly Phe Ser Asp Val Arg Lys Val  
 1 5 10 15  
 Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu  
 20 25 30  
 Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu  
 35 40 45  
 Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile  
 50 55 60  
 Pro Leu Glu Ser Cys Phe Asn Ile Asn Lys Arg Ala Asp Ser Lys Asn  
 65 70 75 80

Lys His Leu Val Ala Leu Tyr Thr Arg Asp Glu His Phe Ala Ile Ala  
                             85                            90                            95

Ala Asp Ser Glu Ala Glu Gln Asp Ser Trp Tyr Gln Ala Leu Leu Gln  
                             100                            105                            110

Leu His Asn Arg Ala Lys Gly His His Asp Gly Ala Ala Ala Leu Gly  
                             115                            120                            125

Ala Gly Gly Gly Gly Gly Ser Cys Ser Gly Ser Ser Gly Leu Gly Glu  
                             130                            135                            140

Ala Gly Glu Asp Leu Ser Tyr Gly Asp Val Pro Pro Gly Pro Ala Phe  
 145                            150                            155                            160

Lys Glu Val Trp Gln Val Ile Leu Lys Pro Lys Gly Leu Gly Gln Thr  
                             165                            170                            175

Lys Asn Leu Ile Gly Ile Tyr Arg Leu Cys Leu Thr Ser Lys Thr Ile  
                             180                            185                            190

Ser Phe Val Lys Leu Asn Ser Glu Ala Ala Ala Val Val Leu Gln Leu  
                             195                            200                            205

Met Asn Ile Arg Arg Cys Gly His Ser Glu Asn Phe Phe Phe Ile Glu  
                             210                            215                            220

Val Gly Arg Ser Ala Val Thr Gly Pro Gly Glu Phe Trp Met Gln Val  
 225                            230                            235                            240

Asp Asp Ser Val Val Ala Gln Asn Met His Glu Thr Ile Leu Glu Ala  
                             245                            250                            255

Met Arg Ala Met Ser Asp Glu Phe Arg Pro Arg Ser Lys Ser Gln Ser  
                             260                            265                            270

Ser Ser Asn Cys Ser Asn Pro Ile Ser Val Pro Leu Arg Arg His His  
                             275                            280                            285

Leu Asn Asn Pro Pro Pro Ser Gln Val Gly Leu Thr Arg Arg Ser Arg  
                             290                            295                            300

Thr Glu Ser Ile Thr Ala Thr Ser Pro Ala Ser Met Val Gly Gly Lys  
 305                            310                            315                            320

Pro Gly Ser Phe Arg Val Arg Ala Ser Ser Asp Gly Glu Gly Thr Met  
                             325                            330                            335



Ser Arg Pro Ala Ser Val Asp Gly Ser Pro Val Ser Pro Ser Thr Asn  
 340 345 350

Arg Thr His Ala His Arg His Arg Gly Ser Ala Arg Leu His Pro Pro  
 355 360 365

Leu Asn His Ser Arg Ser Ile Pro Met Pro Ala Ser Arg Cys Ser Pro  
 370 375 380

Ser Ala Thr Ser Pro Val Ser Leu Ser Ser Ser Thr Ser Gly His  
 385 390 395 400

Gly Ser Thr Ser Asp Cys Leu Phe Pro Arg Arg Ser Ser Ala Ser Val  
 405 410 415

Ser Gly Ser Pro Ser Asp Gly Gly Phe Ile Ser Ser Asp Glu Tyr Gly  
 420 425 430

Ser Ser Pro Cys Asp Phe Arg Ser Ser Phe Arg Ser Val Thr Pro Asp  
 435 440 445

Ser Leu Gly His Thr Pro Pro Ala Arg Gly Glu Glu Glu Leu Ser Asn  
 450 455 460

Tyr Ile Cys Met Gly Gly Lys Gly Pro Ser Thr Leu Thr Ala Pro Asn  
 465 470 475 480

Gly His Tyr Ile Leu Ser Arg Gly Gly Asn Gly His Arg Cys Thr Pro  
 485 490 495

Gly Thr Gly Leu Gly Thr Ser Pro Ala Leu Ala Gly Asp Glu Ala Ala  
 500 505 510

Ser Ala Ala Asp Leu Asp Asn Arg Phe Arg Lys Arg Thr His Ser Ala  
 515 520 525

Gly Thr Ser Pro Thr Ile Thr His Gln Lys Thr Pro Ser Gln Ser Ser  
 530 535 540

Val Ala Ser Ile Glu Glu Tyr Thr Glu Met Met Pro Ala Tyr Pro Pro  
 545 550 555 560

Gly Gly Gly Ser Gly Gly Arg Leu Pro Gly His Arg His Ser Ala Phe  
 565 570 575

Val Pro Thr Arg Ser Tyr Pro Glu Glu Gly Leu Glu Met His Pro Leu  
 580 585 590

Glu Arg Arg Gly Gly His His Arg Pro Asp Ser Ser Thr Leu His Thr  
 595 600 605

Asp Asp Gly Tyr Met Pro Met Ser Pro Gly Val Ala Pro Val Pro Ser  
 610 615 620

Gly Arg Lys Gly Ser Gly Asp Tyr Met Pro Met Ser Pro Lys Ser Val  
 625 630 635 640

Ser Ala Pro Gln Gln Ile Ile Asn Pro Ile Arg Arg His Pro Gln Arg  
 645 650 655

Val Asp Pro Asn Gly Tyr Met Met Met Ser Pro Ser Gly Gly Cys Ser  
 660 665 670

Pro Asp Ile Gly Gly Gly Pro Ser Ser Ser Ser Ser Ser Ser Asn Ala  
 675 680 685

Val Pro Ser Gly Thr Ser Tyr Gly Lys Leu Trp Thr Asn Gly Val Gly  
 690 695 700

Gly His His Ser His Val Leu Pro His Pro Lys Pro Pro Val Glu Ser  
 705 710 715 720

Ser Gly Gly Lys Leu Leu Pro Cys Thr Gly Asp Tyr Met Asn Met Ser  
 725 730 735

Pro Val Gly Asp Ser Asn Thr Ser Ser Pro Ser Asp Cys Tyr Tyr Gly  
 740 745 750

Pro Glu Asp Pro Gln His Lys Pro Val Leu Ser Tyr Tyr Ser Leu Pro  
 755 760 765

Arg Ser Phe Lys His Thr Gln Arg Pro Gly Glu Pro Glu Glu Gly Ala  
 770 775 780

Arg His Gln His Leu Arg Leu Ser Thr Ser Ser Gly Arg Leu Leu Tyr  
 785 790 795 800

Ala Ala Thr Ala Asp Asp Ser Ser Ser Ser Thr Ser Ser Asp Ser Leu  
 805 810 815

Gly Gly Gly Tyr Cys Gly Ala Arg Leu Glu Pro Ser Leu Pro His Pro  
 820 825 830

His His Gln Val Leu Gln Pro His Leu Pro Arg Lys Val Asp Thr Ala  
 835 840 845

Ala Gln Thr Asn Ser Arg Leu Ala Arg Pro Thr Arg Leu Ser Leu Gly  
 850 855 860

Asp Pro Lys Ala Ser Thr Leu Pro Arg Ala Arg Glu Gln Gln Gln Gln  
 865 870 875 880

Gln Gln Pro Leu Leu His Pro Pro Glu Pro Lys Ser Pro Gly Glu Tyr  
 885 890 895

Val Asn Ile Glu Phe Gly Ser Asp Gln Ser Gly Tyr Leu Ser Gly Pro  
 900 905 910

Val Ala Phe His Ser Ser Pro Ser Val Arg Cys Pro Ser Gln Leu Gln  
 915 920 925

Pro Ala Pro Arg Glu Glu Glu Thr Gly Thr Glu Glu Tyr Met Lys Met  
 930 935 940

Asp Leu Gly Pro Gly Arg Arg Ala Ala Trp Gln Glu Ser Thr Gly Val  
 945 950 955 960

Glu Met Gly Arg Leu Gly Pro Ala Pro Pro Gly Ala Ala Ser Ile Cys  
 965 970 975

Arg Pro Thr Arg Ala Val Pro Ser Ser Arg Gly Asp Tyr Met Thr Met  
 980 985 990

Gln Met Ser Cys Pro Arg Gln Ser Tyr Val Asp Thr Ser Pro Ala Ala  
 995 1000 1005

Pro Val Ser Tyr Ala Asp Met Arg Thr Gly Ile Ala Ala Glu Glu Val  
 1010 1015 1020

Ser Leu Pro Arg Ala Thr Met Ala Ala Ala Ser Ser Ser Ser Ala Ala  
 1025 1030 1035 1040

Ser Ala Ser Pro Thr Gly Pro Gln Gly Ala Ala Glu Leu Ala Ala His  
 1045 1050 1055

Ser Ser Leu Leu Gly Gly Pro Gln Gly Pro Gly Gly Met Ser Ala Phe  
 1060 1065 1070

Thr Arg Val Asn Leu Ser Pro Asn Arg Asn Gln Ser Ala Lys Val Ile  
 1075 1080 1085

Arg Ala Asp Pro Gln Gly Cys Arg Arg Arg His Ser Ser Glu Thr Phe  
 1090 1095 1100

Ser Ser Thr Pro Ser Ala Thr Arg Val Gly Asn Thr Val Pro Phe Gly  
 1105 1110 1115 1120

Ala Gly Ala Ala Val Gly Gly Gly Gly Gly Ser Ser Ser Ser Ser Glu  
 1125 1130 1135

Asp Val Lys Arg His Ser Ser Ala Ser Phe Glu Asn Val Trp Leu Arg  
 1140 1145 1150

Pro Gly Glu Leu Gly Gly Ala Pro Lys Glu Pro Ala Lys Leu Cys Gly  
 1155 1160 1165

Ala Ala Gly Gly Leu Glu Asn Gly Leu Asn Tyr Ile Asp Leu Asp Leu  
 1170 1175 1180

Val Lys Asp Phe Lys Gln Cys Pro Gln Glu Cys Thr Pro Glu Pro Gln  
 1185 1190 1195 1200

Pro Pro Pro Pro Pro Pro Pro His Gln Pro Leu Gly Ser Gly Glu Ser  
 1205 1210 1215

Ser Ser Thr Arg Arg Ser Ser Glu Asp Leu Ser Ala Tyr Ala Ser Ile  
 1220 1225 1230

Ser Phe Gln Lys Gln Pro Glu Asp Arg Gln  
 1235 1240

<210> 6  
 <211> 5828  
 <212> DNA  
 <213> Homo sapiens

<400> 6  
 cgggcgcgcg gtcggagggg gccggcgcgcg agagccagac gccgcgcgtt gttttggttg 60  
 gggctctcgg caactctccg aggaggagga ggaggaggga ggaggggaga agtaactgca 120  
 gcggcagcgc cctcccgagg aacaggcgctc ttccccgaac ccttcccaaa cctcccccat 180  
 cccctctcgc ccttgtcccc tccctctctc cccagccgcc tggagcgagg ggcagggatg 240  
 agtctgtccc tccggccggt cccagctgc agtggtgcc cggtatcgtt tgcgatggaa 300  
 aagccacttt ctccaccgc cgagatgggc ccgatgggg ctgcagagga cgcgcccgcg 360  
 ggcggcggca gcagcagcag cagcagcagc agcaacagca acagccgcag cgccgcggtc 420  
 tctgcgactg agctggtatt tgggcggctg gtggcggtg ggacggttg ggggtgggag 480  
 gaggcgaagg aggagggaga accccgtgca acgttgggac ttggcaacct gcctccccct 540  
 gcccagatg atttaatttg cctcgggaat cgctgcttcc agaggggaac tcaggaggga 600  
 aggcgcgcgc gcgcgcgcgc tctggaggg gcaccgcagg gacccccgac tgtcgctctc 660  
 ctgtgccgga ctccagccgg ggcgacgaga gatgcatctt cgctccttcc tgggtggcggc 720  
 ggcggctgag aggagacttg gctctcggag gatcggggct gccctcacc cggacgcact 780  
 gcctccccgc cggcgtaag cggccgaaa ctccggtcgg gctctctctt gggctcagca 840

gctgctcct	ccttcagctg	ccccccccg	gcgcgggggg	cggcgtggat	ttcagagtcg	900
gggtttctgc	tgcctccagc	cctgtttgca	tgtgccgggc	cgcggcgagg	agcctccgcc	960
ccccacccgg	ttgtttttcg	gagcctccct	ctgctcagcg	ttggtggtgg	cgggtggcagc	1020
atggcgagcc	ctccggagag	cgatggcttc	tccgacgtgc	gcaaggtggg	ctacctgcgc	1080
aaaccaaga	gcctgcacaa	acgtttcttc	gtactgcgcg	cggccagcga	ggctggggggc	1140
ccggcgcgcc	tcgagtaeta	cgagaacgag	aagaagtggc	ggcacaagtc	gagcgccccc	1200
aaacgctcga	tcccccttga	gagctgcttc	aacatcaaca	agcgggctga	ctccaagaac	1260
aagcacctgg	tggctctcta	cacccgggac	gagcactttg	ccatcgcggc	ggacagcgag	1320
gccgagcaag	acagctggta	ccaggtcttc	ctacagctgc	acaaccgtgc	taagggccac	1380
cacgacggag	ctgcggccct	cggggcggga	ggtggtgggg	gcagctgcag	cggcagctcc	1440
ggccttggtg	aggctgggga	ggacttgagc	tacggtgacg	tgcccccagg	acccgcattc	1500
aaagaggtct	ggcaagtgat	cctgaagccc	aagggcctgg	gtcagacaaa	gaacctgatt	1560
ggtatctacc	gcctttgcct	gaccagcaag	accatcagct	tcgtgaagct	gaactcggag	1620
gcagcggccg	tgggtgctga	gctgatgaac	atcaggcgct	gtggccactc	ggaaaacttc	1680
ttcttcacat	aggtggggccg	ttctgcctg	acggggcccg	gggagttctg	gatgcagggtg	1740
gatgactctg	tgggtggccca	gaacatgcac	gagaccatcc	tggaggccat	gcggggccatg	1800
agtgatgagt	tccgcctctg	cagcaagagc	cagtcctcgt	ccaactgctc	taaccccatc	1860
agcgtcccc	tgcgcgggca	ccatctcaac	aatccccgc	ccagccaggt	ggggctgacc	1920
cgccgatcac	gcactgagag	catcacgcc	acctccccg	ccagcatggt	gggcgggaag	1980
ccaggtcct	tccgtgtccg	cgcctccagt	gacggcgaag	gcaccatgtc	ccgcccagcc	2040
tcggtggaag	gcagccctgt	gagtcccagc	accaacagaa	cccacgcca	ccggcatcgg	2100
ggcagcggcc	ggctgcaccc	cccgtcaac	cacagccgct	ccatcccat	gccggcttcc	2160
cgctgctcgc	cttcggccac	cagcccggtc	agtctgtcgt	ccagtagcac	cagtggccat	2220
ggctccacct	cggattgtct	cttcccacgg	cgatctagt	cttcgggtgtc	tggttcccc	2280
agcgatggcg	gtttcatctc	ctcgatgag	tatggctcca	gtccctgcga	tttcgggagt	2340
tccttcgca	gtgtcactcc	ggattccctg	ggccacaccc	caccagcccg	cgggtgaggag	2400
gagctaagca	actatatctg	catgggtggc	aaggggccct	ccaccctgac	cgcccccaac	2460
ggtcactaca	ttttgtctcg	gggtggcaat	ggccaccgct	gcaccccagg	aacaggcttg	2520
ggcacgagtc	cagccttggc	tggggatgaa	gcagccagt	ctgcagatct	ggataatcgg	2580
ttccgaaaga	gaactcactc	ggcaggcaca	tccctacca	ttacccacca	gaagaccccg	2640
tcccagtcct	cagtggcttc	cattgaggag	tacacagaga	tgatgcctgc	ctacccacca	2700
ggaggtggca	gtggaggccg	actgccggga	cacaggcact	ccgccttcgt	gcccacccgc	2760
tcctacccag	aggagggtct	ggaaatgcac	cccttgagc	gtcggggggg	gcaccaccgc	2820
ccagacagct	ccaccctcca	cacggatgat	ggctacatgc	ccatgtcccc	aggggtggcc	2880
ccagtgccca	gtggccgaaa	gggcagtggg	gactatatgc	ccatgagccc	caagagcgta	2940
tctgccccac	agcagatcat	caatcccatc	agacgccatc	cccagagagt	ggaccccaat	3000
ggctacatga	tgatgtcccc	cagcgggtggc	tgtctcctg	acattggagg	tggccccagc	3060
agcagcagca	gcagcagcaa	cgcgtccct	tccgggacca	gctatggaaa	gctgtggaca	3120
aacggggtag	ggggccacca	ctctcatgtc	ttgcctcacc	ccaaaccccc	agtggagagc	3180
agcgggtgga	agctcttacc	ttgcacaggt	gactacatga	acatgtcacc	agtggggggac	3240
tccaacacca	gcagcccttc	cgactgtctac	tacggccctg	aggaccccca	gcacaagcca	3300
gtcctctcct	actactcatt	gccaagatcc	tttaagcaca	cccagcgc	cggggagccg	3360
gaggaggggtg	ccggcatca	gcacctccgc	ctttccacta	gctctggtcg	ccttctctat	3420
gctgcaacag	cagatgattc	ttcctcttcc	accagcagcg	acagcctggg	tgggggatac	3480
tgcggggcta	ggctggagcc	cagccttcca	catccccacc	atcaggttct	gcagcccat	3540
ctgcctcgaa	aggtggacac	agctgctcag	accaatagcc	gcctggcccc	gcccacgagg	3600
ctgtccctgg	gggatcccaa	ggccagcacc	ttacctcggg	cccagagcga	gcagcagcag	3660
cagcagccct	tgctgcaccc	tccagagccc	aagagcccgg	gggaatatgt	caatattgaa	3720

```

tttgggagtg atcagtcctgg ctacttgtct ggcccgggtgg ctttccacag ctcaccttct 3780
gtcagggtgc catcccagct ccagccagct cccagagagg aagagactgg cactgaggag 3840
tacatgaaga tggacctggg gccggggccgg agggcagcct ggcaggagag cactgggggc 3900
gagatgggca gactggggccc tgcacctccc ggggctgcta gcatttgcag gcctacccgg 3960
gcagtgcccc gcagccgggg tgactacatg accatgcaga tgagtgtcc ccgtcagagc 4020
tacgtggaca cctcgccagc tggccctgta agctatgctg acatgcgaac aggcattgct 4080
gcagaggagg tgagcctgcc cagggccacc atggctgctg cctcctcatc ctcagcagcc 4140
tctgcttccc cgactggggc tcaaggggca gcagagctgg ctgcccactc gtccctgctg 4200
ggggggccac aaggacctgg gggcatgagc gccttcaccc ggggtgaacct cagtcctaac 4260
cgcaaccaga gtgccaaagt gatccgtgca gaccacaag ggtgccggcg gaggcatagc 4320
tccgagactt tctcctcaac acccagtgcc acccgggtgg gcaacacagt gcccttttga 4380
gcgggggagc cagtaggggg cggtggcggg agcagcagca gcagcgagga tgtgaaacgc 4440
cacagctctg ctctctttga gaatgtgtgg ctgaggcctg gggagcttgg gggagcccc 4500
aaggagccag ccaaactgtg tggggctgct ggggggttgg agaatggtct taactacata 4560
gacctggatt tgggtcaagga cttcaaacag tgccctcagg agtgcacccc tgaaccgcag 4620
cctccccac cccaccccc tcatcaaccc ctgggcagcg gtgagagcag ctccaccgcg 4680
cgctcaagtg aggatttaag cgcctatgcc agcatcagtt tccagaagca gccagaggac 4740
cgtcagtagc tcaactggac atcacagcag aatgaagacc taaatgacct cagcaaatcc 4800
tcttctaact catgggtacc cagactctaa atatttcatg attcacaact aggacctcat 4860
atcttctca tcagtagatg gtacgatgca tccatttcag tttgtttact ttatccaatc 4920
ctcaggattt cattgactga actgcacgtt ctatattgtg ccaagcgaaa aaaaaaatg 4980
cactgtgaca ccagaataat gagtctgcat aaacttcac ttcaacctta aggacttagc 5040
tggccacagt gagctgatgt gcccaccacc gtgtcatgag agaattgggtt tactctcaat 5100
gcattttcaa gatacatttc atctgctgct gaaactgtgt acgacaaagc atcattgtaa 5160
attatttcat acaaaactgt tcacgttggg tggagagagt attaaatatt taacataggt 5220
tttgatttat atgtgtaatt ttttaaataa aaatgtaact tttcttacag cacatctttt 5280
ttttggatgt gggatggagg tatacaatgt tctgttgtaa agagtggagc aaatgcttaa 5340
aacaaggctt aaaagagtag aatagggtat gatccttgtt ttaagattgt aattcagaaa 5400
acataatata agaatcatag tgccatagat ggttctcaat tgtatagtta tatttgctga 5460
tactatctct tgtcatataa acctgatgtt gagctgagtt ccttataaga attaacttta 5520
attttgtatt ttttctgta agacaatagg ccatgttaat taaactgaag aaggatatat 5580
ttggctgggt gttttcaaat gtcagcttaa aattggtaat tgaatggaag caaaattata 5640
agaagaggaa attaaagtct tcattgcat gtattgtaaa cagaaggaga tgggtgattc 5700
cttcaattca aaagctctct ttggaatgaa caatgtgggc gtttgtaaat tctggaaatg 5760
tctttctatt cataataaac tagatactgt tgatctttta aaaaaaaaaa aaaaaaaaaa 5820
aaaaaaaaa

```

<210> 7

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG epitope

<400> 7

Asp Tyr Lys Asp Asp Asp Asp Lys

1

5

<210> 8

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 8

gggggaattt gtcaata

17

<210> 9

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 9

gaatttggtta atattg

16